

```

1 MPARRLLLLLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
1 MPARRLLLLLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50

51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100

101 PELVQASPCRSSDGILYMGGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150
  |||||
101 PELVQASPCRSSDGILYMGGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150

151 TSLLYLGRTEYTIITMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
151 TSLLYLGRTEYTIITMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200

201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250
  |||||
201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250

```

FIG. 1

```

251 RYLTFFMSGVGRITKKWKYPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
251 RYLTFFMSGVGRITKKWKYPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300

301 HEGVAVVPRGSTLPLLEGPTDGVITIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
301 HEGVAVVPRGSTLPLLEGPTDGVITIGDKGECVITPSTDVKFDPGLKSKN 350

351 KLNLYLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKSF 400
|||||
351 KLNLYLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKSF 400

401 EE..TLLQMTS 409
|| :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.¹)

```

5  QLQSVSSAIHLCDKMKMELSLNIPVNHGPQEESCGSSQLHENSGBPETS 54
   :|||||||||||||||||||||||||||||||||||||||||
313 KLQSVSSAIHLCDKMKMELSLNIPVNHGPQEESCGSSQLHENSGBPETS 362

   . . . . .
55  SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSHWDSTISGSQRAAFCDHKT 104
   |||||||||||||||||||||||||||||||||||||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSHWDSTISGSQRAAFCDHKT 412

   . . . . .
105 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTACLNQSLDA 154
   |||||||||||||||||||||||||||||||||||||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTACLNQSLDA 462

   . . . . .
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVI VQKLKDN 204
   |||||||||||||||||||||||||||||||||||||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVI VQKLKDN 512

   .
205 KQMG LQPYPEILVVSRSRPSLNLLQNKSM 232
   |||||||||||||||||||||||||||
513 KQMG LQPYPEILVVSRSRPSLNLLQNKSM 540

```

FIG. 2

FIG. 3

```

1  MGLVSSKKPDKEKPIKEKDKGQWSPLKVS AQDKDAPLPPLVVFNHLTPP 50
   |||||
1  MGLVSSKKPDKEKPIKEKDKGQWSPLKVS AQDKDAPLPPLVVFNHLTPP 50

51 PPDEHLDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100
   |||||
51 PPDEHLDKHFVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARSL 100

101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
   |||||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150

151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYISPRITFPSLQA 200
   |||||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYISPRITFPSLQA 200

201 LVQHYS..... 206
     |||||

201 LVQHYSKKGDLGCQRLTLPCVRPAPQNPWAQDEWEIPRQSLRLVRKLGSG 250

207 .....SYKNNMKVAIKTLKEGTMSPEAFLGEANVMKALQHERLVRLY 249
     :|||||
251 QFGEVWMGYKNNMKVAIKTLKEGTMSPEAFLGEANVMKALQHERLVRLY 300

```

FIG. 4

```

250 AVVTKEPIYIVTEYMARGCLLDFLKKTDEGSRLSLPRLIDMSAQIAEGMAY 299
   |||||||
301 AVVTKEPIYIVTEYMARGCLLDFLKKTDEGSRLSLPRLIDMSAQIAEGMAY 350
   |||||||
300 IERMNSIHRDLRAANILVSEALCCKIADFLARIIDSEYTAQEGAKFPIK 349
   |||||||
351 IERMNSIHRDLRAANILVSEALCCKIADFLARIIDSEYTAQEGAKFPIK 400
   |||||||
350 WTAPEAIHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 399
   |||||||
401 WTAPEAYHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 450
   |||||||
400 GYRMPRPDTCPPELYRGVIAECWRSRPERPTFEFLQSLEDFYTATERQ 449
   |||||||
451 GYRMPRPDTCPPELYRGVIAECWRSRPERPTFEFLQSLEDFYTATERQ 500

```

FIG. 4 (CONT.)

```

1  MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIR 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIR 50

```

FIG. 5

```

1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVVRRCIHKPTSQEYAVKV 50
  |||||
1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVVRRCIHKPTSQEYAVKV 50

51 IDVTGGGSFSPPEVRELREATLKEVDILRKVSGHPNISIQLKDTYETNTF 100
  |||||
51 IDVTGGGSFSPPEVRELREATLKEVDILRKVSGHPNI.IQLKDTYETNTF 99

101 FFLVFDLMKRGELFD 115
  |||||
100 FFLVFDLMKRGELFD 114

```

FIG. 6

FIG. 7

```

22  AVGCILAE1LLAHR2PL3LP4GTSE5IHQ6IDL7IVQ8LLGTP9SENI10WPG11FSKL12PL13VG 71
    |||||14|||||15|||||16|||||17|||||18|||||19|||||20|||||21|||||22|||||23
197 AVGCILAE24LLAHR25PL26LP27GTSE28IHQ29IDL30IVQ31LLGTP32SENI33WPG34FSKL35PL36VG 246
    |||||37|||||38|||||39|||||40|||||41|||||42|||||43|||||44|||||45
    .
72  QYSLRKQ46PYNN47LKH48KFP49WLSEAG50RL51LLH52FLF53MYD54PKK55RATAG56DCLE57SSYF 121
    |||||58|||||59|||||60|||||61|||||62|||||63|||||64|||||65|||||66|||||67
247 QYSLRKQ68PYNN69LKH70KFP71WLSEAG72RL73LLH74FLF75MYD76PKK77RATAG78DCLE79SSYF 296
    .
    122 KEKPLRLPISGVCEGCREPG 141
        |||||142|||||143|||||144|||||145
    297 KEKPLRLPISGVCEGCREPG 316

```

FIG. 8

```
1 VFLGRCRSVKFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEK 50
  |||||
1 VFLGRCRSVKFEKLNRI GEGTYGIVYRARDTQTDEI VALKKVRMDKEK 50

      .
51 GIPSSLREITLLRLRHPNIV 72
   |||||
51 GIPSSLREITLLRLRHPNIV 72
```

FIG. 9

```

1  MGEAEKFHYIYSCDL DINVQLKIGSLEGRQKSYKAVLEDPMLKFSGLY 50
  |||||
1  MGEAEKFHYIYSCDL DINVQLKIGSLEGRQKSYNAVLEDPMLKFSGLY 50
  |||||
51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
  |||||
51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
  |||||
101 PRNAQVALTIWDVYGPGKAVPVGGTTVSLFGKYGMFRQGMHDLKVWP NVE 150
  |||||
101 PRNAQVALTIWDVYGPGKAVPVGGTTVSLFGKYGMSRQGMHDLKVWP NVE 150
  |||||
151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLT FRE 200
  |||||:|||||
151 ADGSEPTNTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLT FRE 200
  |||||
201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVVYEKDGDESSPILTS F 250
  |||||
201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVVYEKDGDESSPILTS F 250
  |||||
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGPSDHDCLKPYSPRDQLKNIV 300
  |||||
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGPSDHDCLKPYSPRDQLKNIV 300
  |||||

```

FIG. 10

551	RLVHLMKAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK	600
551	RLVHLMKAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK	600
601	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRRQDLILQI	650
601	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRRQDLILQI	650
651	ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTEGSI	700
651	ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTEGSI	700
701	QNFFRKYPSENGPNGISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL	750
701	QNFFRKYPSENGPNGISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLLV	750
	751 LTKTG 755	
	751 LTKTG 755	

FIG. 10 (CONT.²)

1 MGEAEKFHYIYSCDLINVLKIGSLEKREQKSYKAVLEDPMLKFSGLY 50
 |||||
 1 MGEAEKFHYIYSCDLINVLKIGSLEKREQKSYNAVLEDPMLKFSGLY 50
 |||||
 51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNNEWLKLVPKYPD 100
 |||||
 51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNNEWLKLVPKYPD 100
 |||||
 101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMFRQGMHDLKVWP 150
 |||||
 101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMSRQGMHDLKVWP 150
 |||||
 151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLT 200
 |||||
 151 ADGSEPTKTPGRTSS TLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLT 200
 |||||
 201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILT 250
 |||||
 201 IEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILT 250
 |||||
 251 ELVKVPDPQMSLENLVESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300
 |||||
 251 ELVKVPDPQMSLENLVESKHHNLPRLSRGPSDHD LKPYSPRDQLKNIV 300

FIG. 11

FIG. 12

FIG. 13

FIG. 14


```

21 KSGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 70
   ::|||||
295 EKGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 344

71 GGSVIKYSKNTTRKQWLKETPDTLLNILKNADLSLAFQTYTYIRPGSEGF 120
   |||||||
345 GGSVIKYSKNTTRKQWLKETPDTLLNILKNADLSLAFQTYTYIRPGSEGF 394

121 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFFEEEDDNPDWV 170
   |||||||
395 LKGPLSEETEASDSVDGGHDSVILDPERLEPGLDEEDTDFFEEEDDNPDWV 444

171 SELKKRAGWQGLCDR 185
   |||||||
445 SELKKRAGWQGLCDR 459

```

FIG. 16

```

1  MAPPEETPLIPQRCSLLSTEAGALHVLLPARCGPPQRLSFG 46
  | | | | | | | | | | | | | | | | | | | | | | | |
1  MAPPEETPLIPQRCSLLSTEAGALHVLLPARCGPPQRLSFG 46

```

FIG. 17

```

1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50
  |||||
1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50

. . .
51 ACMVSI FNL DGM EHH VRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100
  |||||
51 ACMVSI FNL DGM EHH VRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100

. . .
101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLLFLIIIVFLVIN 150

. . .
151 YHQRVYHNRRQLDMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGTKFF 198
  ||||| :|
151 YHQRVYHNRRQLDMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGLPLF 198

```

FIG. 18

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
|||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
|||||
51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQSAGD 150
|||||
101 DKAIDILDRSSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQSAGD 150
151 INTIYQPPEPRSRHLSVSSQNPGRSSPPGYVPERQQHARQGSYTSINS 200
|||||
151 INTIYQPPEPRSRHLSVSSQNPGRSSPPGYVPERQQHARQGSYTSINS 200
201 EGEFIPETSEQCMLDPLSSAENSLGSCQSLDRSADSPSFRKSRMSRAQS 250
|||||
201 EGEFIPETSEQCMLDPLSSAENSLGSCQSLDRSADSPSFRKSRMSRAQS 250

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300
|||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFPRIRR 300

301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRILRSADSENALSVQERN 350
|||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRILRSADSENALSVQERN 350

351 VPTKCEELSLARRRLPRWSQTSYGGKQLG 379
|||| : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

FIG. 20

```

251 AENSLGSCQSLDRSADSPFRKSRMSRAQFFPDNRQEYSDRETQLYDKG 300
    |||||||
220 AENSLGSCQSLDRSADSPFRKSRMSRAQFFPDNRQEYSDRETQLYDKG 269
    .
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 350
    |||||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 319
    .
351 ENMGLAVQYLDPRGRLSADSENALSVQERNVPTKCEELSLARRRLPRWS 400
    |||||||
320 ENMGLAVQYLDPRGRLSADSENALSVQERNVPTKSPSAPINWRR..... 364
    .
    401 QTSYGGKQLG 410
        || ||
    365 .....GKLLG 369

```

FIG. 20 (CONT.¹)

```

1 MAKQYDSVECPFCDEVSKYEKLAKIGQGTGFEVFKARHRKTGQKVALKKV 50
  |||||
1 MAKQYDSVECPFCDEVSKYEKLAKIGQGTGFEVFKARHRKTGQKVALKKV 50
      .
51 LMENEKEGPITALREIKILQLLKHENVVNLIEICRTKASPNRCKGSY 100
  |||||
51 LMENEKEGPITALREIKILQLLKHENVVNLIEICRTKASPNRCKGSY 100
      .
101 LVDFECEHDLAGLLSNVLVKFTLSEIKRVMQMLNGLYY..... 139
  |||||
101 LVDFECEHDLAGLLSNVLVKFTLSEIKRVMQMLNGLYYIHRNKILHRDM 150
      .
139 ..... 139
      .
151 KAA NVLI TRDGV LKLA DFG LARA FSLAK NSQPNRY TNRVVTLWYRPP ELL 200
      .
139 ..... 139
201 LGERDYGPPI DLWGAGC IMAEMWTRSPIMQGNTEHQHQLALISQLCGSITP 250
      .

```

FIG. 21

FIG. 21 (CONT.¹)

FIG. 23


```

34  PLPLEPRAVYCKDVL DIEQFSTVKG VNL DHTDD FYSKFSTGSVIPWQ N 83
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
464 PFVPDPRAVYCKDVL DIEQFSTVKG VNL DHTDD FYSKFSTGSVIPWQ N 513
   .
   .
84  EMIETECFKELNVFGPN GTLP PDLNRNHPPEPPKKGLLQRLFKRQHQN NS 133
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
514 EMIETECFKELNVFGPN GTLP PDLNRNHPPEPPKKGLLQRLFKRQHQN NS 563
   .
   .
134 KSSPSSKTSFNHHINS NHVSSNSTGSS 160
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
564 KSSPSSKTSFNHHINS NHVSSNSTGSS 590

```

FIG. 24

```

28  LLSPSGHIRISDLGLAVKIPEGLIRGRVGTGYMAPEVLNNQRYGLSPD 77
   ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LLDDYGHIRISDLGLAVKIPEGLIRGRVGTGYMAPEVLNNQRYGLSPD 367

   . . . . .
78  YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEAK 127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEAK 417

   . . . . .
128 SICKMLLTAKQRLGCQEEGAAEVKRHPFFRNMNFKRLEAGMLDPPFVP 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 SICKMLLTAKQRLGCQEEGAAEVKRHPFFRNMNFKRLEAGMLDPPFVP 467

   . . . . .
178 DPRVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVSIPWQNE MIE 227
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 DPRVYCKDVL DIEQFSTVKGVNLDHTDDDFYSKFSTGSVSIPWQNE MIE 517

   . . . . .
228 TECFKELNVFGPNGTLPDLNRNHPPEPPKKGLLQRLFKRQHQNNSKSSP 277
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
518 TECFKELNVFGPNGTLPDLNRNHPPEPPKKGLLQRLFKRQHQNNSKSSP 567

   . . . . .
278 SSKTSFNHHHINSNHVSSNSTGSS 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 SSKTSFNHHHINSNHVSSNSTGSS 590

```

FIG. 25

FIG. 26

[illegible]

FIG. 27

1 MDETHPGYGKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
|||||
203 MDETHPGYGKEVD.....LWACG 220
51 VILFTLLAGSPFWHRRQILMLRMIMEGQYQFSSPEWDDRSSTVKDLISR 100
|||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGQYQFSSPEWDDRSSTVKDLISR 270
101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 150
|||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 320
151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKGEQQNR 200
|||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKGEQQNR 370
201 AALFQHRPPGPPFIMGPEEEGDSAAITDEAVLVG 236
|||||
371 AALFQHRPPGPPFIMGPEEEGDSAAITDEAVLVG 406

FIG. 28

FIG. 29 (CONT.)¹⁾

FIG. 30


```

1  MGCVQCKDKEATKLTEERDGSLNQSSGYRYGTDPTPQHYPFSGVTSIPNY 50
  |||||
1  MGCVQCKDKEATKLTEERDGSLNQSSGYRYGTDPTPQHYPFSGVTSIPNY 50
  .
51 NNFHAAGGQGLTVFGGVNSSSHTGLRTRGGTGVTLFVALYDYEARTEDD 100
  |||||
51 NNFHAAGGQGLTVFGGVNSSSHTGLRTRGGTGVTLFVALYDYEARTEDD 100
  .
101 LSFHKGEKFQILNSSEGDWWEARSILTTGETGYIPSNYVAPVDSIQAEFWY 150
  |||||
101 LSFHKGEKFQILNSSEGDWWEARSILTTGETGYIPSNYVAPVDSIQAEFWY 150
  .
151 FGKLGRKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200
  |||||
151 FGKLGRKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200
  .
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
  |||||
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
  .

```

FIG. 31

251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300
|||||
251 PRLDLSVKT KD VWEI PRES LQLIKRLGNGQFGEVWMGTWNGNTKVAIKT 300
301 LKPGTMSPE SFL EEAQIMKKLKHDKLVQLYAVVSEEP IYI VTEYMNKG 348
|||||
301 LKPGTMSPE SFL EEAQIMKKLKHDKLVQLYAVVSEEP IYI VTEYMNKG 348

FIG. 31 (CONT.¹)

```

50  S L L E L H K R R K A L T E P E A R Y Y L R Q I V L G C Q Y L H R N R V I H R D L K L G N L F L N E      99
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
137 S L L E L H K R R K A L T E P E A R Y Y L R Q I V L G C Q Y L H R N R V I H R D L K L G N L F L N E      186

    . . . . .
100 D L E V K I G D F G L A T K V E Y D G E R K K T L C G T P N Y I A P E V L S K K G H S F E V D V W S      149
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
187 D L E V K I G D F G L A T K V E Y D G E R K K T L C G T P N Y I A P E V L S K K G H S F E V D V W S      236

    . . . . .
150 I G C I M Y T L L V G K P P F E T S C L K E T Y L R I K K N E Y S I P K H I N P V A A S L I Q K M L      199
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
237 I G C I M Y T L L V G K P P F E T S C L K E T Y L R I K K N E Y S I P K H I N P V A A S L I Q K M L      286

    . . . . .
200 Q T D P T A R P T I N E L L N D E F F T S G Y I P A R L P I T C L T I P P R F S I A P S S L D P S N      249
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
287 Q T D P T A R P T I N E L L G D E F F T S G Y I P A R L P I T C L T I P P R F S I A P S S L D P S N      336

    . . . . .
250 R K P L T V L N K G L E N P L P E R P R E K E E P V V R E T G E V V D C H L S D M L Q Q L H S V N A      299
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
337 R K P L T V L N K G L E N P L P E R P R E K E E P V V R E T G E V V D C H L S D M L Q Q L H S V N A      386

```

FIG. 32

```

300 SKPSERGLVRQEEAEDPACIPFVWSKWVDYSKYGLGYQLCDNSVGVLFF 349
|||||
387 SKPSERGLVRQEEAEDPACIPFVWSKWVDYSKYGLGYQLCDNSVGVLFF 436
. . . . .
350 NDSTRILLYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 399
|||||
437 NDSTRILLYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 486
. . . . .
400 SEHLLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
|||||:|||||
487 SEHLLKAGGNITPRQGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
. . . . .
450 DHTKLILCPLMAAVTYIDEKRDFRTYRLSLLEEEYGCKKELASRLRYARTM 499
|||||
537 DHTKLILCPLMAAVTYIDEKRDFRTYRLSLLEEEYGCKKELASRLRYARTM 586
.
500 VDKLLSSRSASNRLKAS 516
|||||
587 VDKLLSSRSASNRLKAS 603
    
```

FIG. 32 (CONT.¹)


```

32  ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
    |: :: ::||:  ||||| ||||| ||||| ||||| ||||| |||||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279
    .
    82  QGFSYDYVFDWNMLKFGASSSQAQPRD 108
        ||||| ||||| ||||| : |:|
    280 QGFSYDYVFDWNMLKFGAARN...PED 303

```

FIG. 34

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPELPGGDDLKS 216
|||||
1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPELPGGDDLKS 50
217 PEEKKTATQLHSKRRPK 233
|||||:|||||
51 PEEKKTTTQLHSKRRPK 67

FIG. 36

.....

FIG. 37

FIG. 37 (CONT.)¹

```

1 MSAKVRLLKKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50
  |||||
1 MSAKVRLLKKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECSHSALRRDK 50

. . . . .
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVKMKNTER 100
  |||||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVKMKNTER 100

. . . . .
101 IYAMKILNKKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||||
101 IYAMKILNKKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

. . . . .
151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLDAIDSIHQLHYVHRD 200
  |||||
151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLDAIDSIHQLHYVHRD 200

. . . . .
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
  |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

```

1 MELRVGNRYRLGRKIGSGSFGDIYL..... 25
  |||||
1 MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVTKHPQLH 50
  .
26 .....VGIP TIRWC GAEGDYNVMVMELLGPSLEDLNFCSRKF 63
  |||||
51 IESKIYKMMQGGVGIP TIRWC GAEGDYNVMVMELLGPSLEDLNFCSRKF 100
  .
64 SLKTVLLLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 113
  |||||
101 SLKTVLLLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 150
  .
114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 163
  |||||
151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 200
  .
164 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 213
  |||||
201 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 250

```

FIG. 39

[illegible]FIG. 39 (CONT.¹)

```

14 TFAAPSFDDKILEVVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 63
   |||||
817 TFAAPSFDDKILEVVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 866

   . . . . .
64 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEQKQKCEL 113
   |||||
867 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEQKQKCEV 916

   . . . . .
114 PRPPSCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMEQELA 163
   |||||
917 PRPPSCSLHPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMEQELA 966

   . . . . .
164 HAVNASSKSMDRVYGKPRTTTEGLNCSEFVLEMVNNFRALRSETELLSGKM 213
   |||||
967 HAVNASSKSMDRVYGKPRTTTEGLNCSEFVLEMVNNFRALRSETE.LLSGKM 1015

   . . . . .
214 ALQLDPPQKEQLGSALAEMDRQLRRIADTPWLCQSAEPGDEESVMLDLAK 263
   |||||
1016 ALQLDPPQKEQLGSALAEMDRQLRRIADTPWLCQSAEPGDEESVMLDLAK 1065

```

FIG. 40

364 AVEA 367

1166 AVEA 1169

FIG. 40 (CONT.¹)

FIG. 42

FIG. 42 (CONT.¹)

14	GEVDLTALAKELRAVEDVRPPHKVTDYSSSSSEESGTTDEEDDDVEQEGAD	63
674	GEVDLTALAKELRAVEDVRPPHKVTDYSSSSSEESGTTDEEDDDVEQEGAD	723
64	ESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIV	113
724	ESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIV	773
114	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	163
774	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	823
164	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	213
824	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	873
214	NLLVGTESGLMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISGKKD	263
874	NLLVGTESGLMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISGKKD	923
264	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	313
924	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	973

FIG. 43

314	VIALKSSVEVYAWAPKPYHKFMFAKSFGE	LVDLTVEEGQRLKVI	363
974	VIALKSSVEVYAWAPKPYHKFMFAKSFGE	LVDLTVEEGQRLKVI	1023
364	YGSCAGFHAVDVGSGSVYDIYLPTHIQCSI	KPHAIILPNTDGMELLVCY	413
1024	YGSCAGFHAVDVGSGSVYDIYLPTHIQCSI	KPHAIILPNTDGMELLVCY	1073
414	EDEGVYVNTYGRITKDVVLQWGEMPTSVAY	IRSNQTMGWGEKAIEIRSVE	463
1074	EDEGVYVNTYGRITKDVVLQWGEMPTSVAY	IRSNQTMGWGEKAIEIRSVE	1123
464	TGHLDGVMHKRAQRLKFLCERNDKVFFASV	RSGSSQVYFMTLGRTSLL	513
1124	TGHLDGVMHKRAQRLKFLCERNDKVFFASV	RSGSSQVYFMTLGRTSLL	1173
	514	SW	515
	1174	SW	1175

FIG. 43 (CONT.¹)

FIG. 44

FIG. 44

314	KVIYGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL	363
1021	KVIYGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELL	1070
364	VCYEDEGVYVNTYGRITKDVVLQWGE MPTSVAYIRSNQTMGWGEKAIEIR	413
1071	VCYEDEGVYVNTYGRITKDVVLQWGE MPTSVAYIRSNQTMGWGEKAIEIR	1120
414	SVETGHL DGVFMHKRAQRLKFLCERN DKVFFASVRS GGSSQVYFMTLGR T	463
1121	SVETGHL DGVFMHKRAQRLKFLCERN DKVFFASVRS GGSSQVYFMTLGR T	1170
	464 SLLSW	468
	1171 SLLSW	1175

FIG. 44 (CONT.¹)

```

1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50

51 GWEIISGVDEHYTPIRTYQVCNVMDHSDQNNWLRTNWVPRNSAQKIYVELK 100
  |||||
51 GWEIISGVDEHYTPIRTYQVCNVMDHSDQNNWLRTNWVPRNSAQKIYVELK 100

101 FTLRDCNSIPLVLGTCKETFNLYMESDDDHGVKFRHQFTKIDTIAADE 150
  |||||
101 FTLRDCNSIPLVLGTCKETFNLYMESDDDHGVKFRHQFTKIDTIAADE 150

151 SFTQMDLGDRIKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200
  |||||
151 SFTQMDLGDRIKLNTEIREVGPVNKKGFYLAQDVGACVALSVRVYFK 200

201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNNSKEEDPPRMYCSTEGEW 250
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNNSKEEDPPRMYCSTEGEW 250
    
```

FIG. 45

FIG. 45 (CONT.¹)


```

501 PDIIYVFQIRARTAAAGYGTSNRKFEFFETSPDSFSISGESSQVVMIAISAA 550
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 PDIIYVFQIRARTAAAGYGTSNRKFEFFETSPDSFSISGESSQVVMIAISAA 550

551 VAIILLTVVIYVLIGRFCGYKS KHGADEKRLHFGNGHLKLPLGLRTYVDPH 600
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551 VAIILLTVVIYVLIGRFCGYKS KHGADEKRLHFGNGHLKLPLGLRTYVDPH 600

        .
        601 TYEDPTQAVHEFAKELDATNISIDKVVG A 629
            | | | | | | | | | | | | | | | | | | | | | |
        601 TYEDPTQAVHEFAKELDATNISIDKVVG A 629

```

FIG. 45 (CONT.)²

FIG. 46

FIG. 46 (CONT.¹)

```

1 MEVVDPPQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIGKYL 50
  |||||
1 MEVVDPPQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIGKYL 50
  . . .
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  . . .
101 LLRRLRHKNVIQLVLDVLYNEEKQKMYMMEYCVCGMQEMLDSVPEKRFV 150
  |||||
101 LLRRLRHKNVIQLVLDVLYNEEKQKMYMMEYCVCGMQEMLDSVPEKRFV 150

151 CQAHG 155
   |||||
151 CQAHG 155

```

FIG. 47

1 MEVDPQQLGMFTEGELMSGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50
 |||||
 1 MEVDPQQLGMFTEGELMSGMDTFIHRIDSTEVYQPRRKRAKLIKYL 50
 51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
 |||||
 51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
 101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFVP 150
 |||||
 101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFVP 150
 151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIKPGNLLLTGGTLKISDLGVAE 199
 |||||
 151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIKPGNLLLTGGTLKISDLGVAE 199

FIG. 48

27 VKDFLSQLRSSNRRFSIPESGQGGTMDGFRRTIENQHSRNDVMVSEWLN 76
|||||:|||||
301 VKDFLSQLKSSNRRFSIPESGQGGTMDGFRRTIENQHSRNDVMVSEWLN 350
77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 126
|||||
351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 400
127 TSTFRNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
|||||
401 TSTFRNQMPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450
177 NIYNCSGVQVGDNNYLTMQTTALPTWGLAPSGKGRGLQHPPPVGSQEGP 226
|||||
451 NIYNCSGVQVGDNNYLTMQTTALPTWGLAPSGKGRGLQHPPPVGSQEGP 500
227 KDPEAWSRPQGWYNHSGK 244
|||||
501 KDPEAWSRPQGWYNHSGK 518

FIG. 49

FIG. 50

```

1  MRLTLCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50
  |||||
1  MRLTLCCTWREERMGEESGSELPVCASCGQRIYDGQYLQALNADWHADCF 50

51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 ELKYHPECFICLTGCTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||||
101 ELKYHPECFICLTGCTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200
  |||||
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200

201 VQGVDPGCMSPDVKN SIHVGDRIEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||
201 VQGVDPGCMSPDVKN SIHVGDRIEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51


```

251 QLTLEHDPHDTLGHGLPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
    |||||
251 QLTLEHDPHDTLGHGLPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
    |||||

301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGCF 350
    |||||
301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGCF 350

351 GQAIKV 356
    |||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

```

      . . . . .
1  MRLTLCCTWREERMGEELPVCASCGQRIYDGQYLQALNADWHADCF 50
      |||||
1  MRLTLCCTWREERMGEELPVCASCGQRIYDGQYLQALNADWHADCF 50

      . . . . .
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
      |||||
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

      . . . . .
101 ELKYHPECFICLTGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
      |||||
101 ELKYHPECFICLTGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

      . . . . .
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCCGTEHSHTVR 200
      |||||
151 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCCGTEHSHTVR 200

      . . . . .
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLIIQETSRL 250
      |||||
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLIIQETSRL 250

```

FIG. 51

```

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300

301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350
|||||
301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350

```

351 GQAIKV 356

Figure 6

351 GQAIKV 356

FIG. 51 (CONT.¹)

[illegible]

FIG. 52

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FIG. 52 (CONT.¹)

1	MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL	50
1	MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL	50
51	KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHQQQLQELHAHVVL	100
51	KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHQQQLQELHAHVVL	100
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQKQGAENMIQ	150
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQKQGAENMIQ	150
151	TYSNGSTKDRKLLLTAAQQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD	200
151	TYSNGSTKDRKLLLTAAQQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD	200
201	DTQGSPDLGAVELRIEELRHFFRVEHAHAEGAKNVLRLLSAAKAPDRKAV	250
201	DTQGSPDLGAVELRIEELRHFFRVEHAHAEGAKNVLRLLSAAKAPDRKAV	250

FIG. 53

FIG. 53 (CONT.²)

FIG. 53 (CONT.²)


```

      . . . . . 723
723 ..... 723
      . . . . . 800
751 EGYVKIADFGLCKEGMGYDRTSTFCGTPEFLAPEVLTDTSYTRAVDWWG 800
      . . . . . 723
723 ..... 723
      . . . . . 850
801 LGVLLYEMLVGESPFPGDDDEEVFDSIVNDEVRYPRFLSAEAI GIMRRLL 850
      . . . . . 738
724 .....RLPPPFPVPTLSGRTD 738
      | | | | |
851 RRNPERRLGSSERDAEDVKKQPFRTLGWEALLARRLPPPFPVPTLSGRTD 900
      . . . . . 780
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 780
      | | | | |
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDFVAGGC 942

```

FIG. 53 (CONT.³)

```

1 MASDAVQSEPRSWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRSWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

.
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

.
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

.
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200

.
201 DTQGSDDLGAVELRIEELRHHFRVEHVAEAGAKNVLRLLSAAKAPDRKAV 250
  |||||
201 DTQGSDDLGAVELRIEELRHHFRVEHVAEAGAKNVLRLLSAAKAPDRKAV 250

```

FIG. 54

251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
251	SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF	300
301	STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNTPSMGG	350
301	STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNTPSMGG	350
351	PGTPDSRPPFLSRPARGLYSRSGLSGRSSIKAEAEENTSEVSTVLKLDNT	400
351	PGTPDSRPPFLSRPARGLYSRSGLSGRSSIKAEAEENTSEVSTVLKLDNT	400

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FIG. 54 (CONT.¹)

FIG. 55

90 LSGASPFGLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 139
|||||
211 LSGASPFGLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 260
|||||
140 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTRLKEYTIKSH 189
|||||
261 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTRLKEYTIKSH 310
|||||
190 SSLPPNNSYADFERFSKVL EEA AAEGLRELQSRRLCHEDVEALAAIY 239
|||||
311 SSLPPNNSYADFERFSKVL EEA AAEGLRELQSRRLCHEDVEALAAIY 360
|||||
240 EEKEAWYREESDSLGGDLRRLRQELLKTEALKRQAQEEAKGALLGTSGLK 289
|||||
361 EEKEAWYREESDSLGGDLRRLRQELLKTEALKRQAQEEAKGALLGTSGLK 410
|||||
290 RRFSLRNRYEALAKQVASEMRVFQDLVRALEQEKLGVECCGLR 333
|||||
411 RRFSLRNRYEALAKQVASEMRVFQDLVRALEQEKLGVECCGLR 454

FIG. 56

FIG. 57

```

1 MRGAARLGRPGRSCLPGPALRAPRPPPLLLLALLPLLPAGAAAAPAPR 50
  |||||
1 MRGAARLGRPGRSCLPGPALRAAAP..ALLARCAVAAAAGLRAAARPR 48
  |||||

51 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFSLL 100
  |||||
49 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFNLL 98
  |||||

101 VPSETNFLHFTWHAKSKVEYKLGQVDNVLAMDMPQVNISVQGEVPRTLS 150
  |||||
99 VPSETNFLHFTWHAKSKVEYKLGQVDNVLAMDMPQVNISVQGEVPRTLS 148
  |||||

151 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMKYKKLEEV 200
  |||||
149 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMKYKKLEEV 198
  |||||

201 KTSALDKNTSRTIYDPVHAAPTSTTRVFYISVGVCCAVIFLVAIILAVLH 250
  |||||
199 KTSALDKNTSRTIYDPVHAAPTSTTRVFYISVGVCCAVIFLVAIILAVLH 248
  |||||

251 LHSMKRIELDD 261
  ||:|||||
249 LHNMKRIELDD 259

```

FIG. 58

```

1  MPQVNISVQGEVPRTLVSFRVELSCTGKVDSEVMILMQLNLTVNSSKNFT 50
   |||||
132 MPQVNISVQGEVPRTLVSFRVELSCTGKVDSEVMILMQLNLTVNSSKNFT 181
   |||||

51  VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTTSTRVFIYSVG 100
   |||||
182 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTTSTRVFIYSVG 231
   |||||

101 VCCAVIFLVAIILAVLHLHSMKRIELDDSIASSSSQGLSQPSTQTQYL 150
   |||||
232 VCCAVIFLVAIILAVLHLHNMKRIELDDSIASSSSQGLSQPSTQTQYL 281
   |||||

151 RADTPNNATPITSSYYPTLRIEKNDLRSVTLLLEAKGKVKDIAISRERITL 200
   |||||
282 RADTPNNATPITS..YPTLRIEKNDLRSVTLLLEAKGKVKDIAISRERITL 329
   |||||

201 KDVLEQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 250
   |||||
330 KDVLEQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 379

```

FIG. 59

251 CKLRGLHHRNLLPITHVCI E E G E K P M V I L P Y M N W G N L K L F L R Q C K L V E A N 300
|||||
380 CKLRGLHHRNLLPITHVCI E E G E K P M V I L P Y M N W G N L K L F L R Q C K L V E A N 429
301 NPQ A I S Q Q D L V H M A I Q I A C G M S Y L A R R E V I H K D L A A R N C V 340
|||||
430 NPQ A I S Q Q D L V H M A I Q I A C G M S Y L A R R E V I H K D L A A R N C V 469

FIG. 59 (CONT.¹)

```

1  MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 50
    |||||||
484 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 533
    .
51  PSPRATDPPSHL.....DGPPAVAVGQCPLVGP.GPMHRRHL 86
    |||||||:
534 PSPRATDPPSHMAPRPWLWASARWGWQAPCTAATCCSLPGSLGLAYRR.. 581
    .
87  LLPARVP...RPGLEALSLLFAVVLSRAAALGCIGLVAHAGQLTAVWR 133
    | | | | | |||:| ||| | ||| |
582 .....RFPCSCSP.....LFCLVPPPPWAALGWWTPTANSPQ..... 612

134 RPGAARAP 141
    |||: |
613 .SGAAQEP 619
    
```

FIG. 60

```

1  MELQAEGATAVTGVSPRATDPPSHL.....DGPPAVAVGQ 37
   |||||
519 MELQAEGATAVTGVSPRATDPPSHMAPRPWLWASARWGWQAPCTAATC 568
      ||::|:
38  CPLVGP.GPMHRRHLLPARVP...RPGLSEALSLLFAVVLSRAAALGC 83
   ||| | | :|| | | | | | | | | | | | | | | |
569 CSLPGSLGLAYRR.....RFPCSCSP.....LFCLVPPPPWAALGW 603
      .
      84  IGLVAHAGQLTAVWRRRPGAARAP 106
          |::| | |||: |
      604 WPTPANSPQ.....SGAAQEP 619

```

FIG. 61

```

6  HEDFEFISGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA  50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
580 HEDFEFIFILGTRMRKLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA  624

```

FIG. 62

FIG. 63

```
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDDVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDDVDLPYP 50
  |||||
51 LNNFSVASSVMFR 63
  |||||: :::
51 LNNFSVAKCQLMK 63
```

FIG. 64

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDVDPYP 50
|||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLCLKTDGSFIGYKEKPQDVDPYP 50
51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPPEEREETE 100
|||||
51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPPEEREETE 100
101 AIQAVADRLQRQEEERMNCSPSTQIDNIGEEEMDASTTHHKRKTMNDFDY 150
|||||
101 AIQAVADRLQRQEEERMNCSPSTQIDNIGEEEMDASTTHHKRKTMNDFDY 150
151 LKLLGKGTFGKVILVREKASGYAMKILKKEVIAK 187
|||||
151 LKLLGKGTFGKVILVREKASGYAMKILKKEVIAK 187

FIG. 65

```

73 SSQYGDRCFMFVLISPTKSVIITILSLFTLQLFFHLSRERVSEDRTR 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
214 SFQTKDRLCFVMEYVNGG.....ELFFHLSRERVSEDRTR 249

123 FYGAEIVSALDYLSHGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITD 172
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
250 FYGAEIVSALDYLSHGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITD 299

173 AATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQ 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
300 AATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQ 349

223 DHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDDAKEI 272
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
350 DHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGGPDDAKEI 399

273 MRHSFFSGVNWQDVYDKKLVPPEKPKQVTSETDTRYFDEEFTAQITITPP 322
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
400 MRHSFFSGVNWQDVYDKKLVPPEKPKQVTSETDTRYFDEEFTAQITITPP 449

323 EKYDEDGMDCMDNERRRPHFPQFSYSASGRE 352
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
450 EKYDEDGMDCMDNERRRPHFPQFSYSASGRE 479

```

FIG. 66


```

1  MELLRTITYQPAASTKMCEQALGKCGGNSKKRPPQPPFESQPPQSQAQ  50
  |||||||
1  MELLRTITYQPAASTKMCEQALGKCGGDSKKRPPQPPFESQPPQSQAQ  50
  |||||||
51 VPAAAPHHHHHSHSGPEISRIIVDPPTTGKRYCRGKVLGKGGFACCYEMT  100
  |||||||
51 VPAAAPHHHHHSHSGPEISRIIVDPPTTGKRYCRGKVLGKGGFACCYEMT  100
  |||||||
      . . .
101 DLTNKKVYAAKIIPHRSVAKPHQREKVCMTLE  132
      |||||||
101 DLTNKKVYAAKIIPHRSVAKPHQREKIDKEIE  132

```

FIG. 67

```

1 MELLRTITYQPAASTKMCEQALGKGCGGNSKKRPPQPPESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGKGCGGDSKKRPPQPPESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYSRR..VSVNSYLRTFAYPELTWYSKSI LSGI 191
  |||||
151 DKENIYILLEYSRRSMAHILKARKVLTEPEVRYLRQIVSGL 193

```

FIG. 68

```

1 MELLRTITYQPAASTKMCEQALGKCGGNSKKRPPQPPEESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGKCGGDSKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
51 VPPAAPHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYSRR 165
  |||||
151 DKENIYILLEYSRR 165

```

FIG. 69

```

1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50
  |||||
1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50

51 ILCHEQQDREEAQREADMHRLFNHPNIIRLVAYCLRERGAKHEAWLLLPF 100
  |||||
51 ILCHEQQDREEAQREADMHRLFNHPNIIRLVAYCLRERGAKHEAWLLLPF 100

```

101 FK 102

101 FK 102

FIG. 70

```

1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAEAAFG LGAAA 50
  |||||
1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAEAAFG LGAAA 50

51 APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEPRGPEPDDETELRPR 100
  |||||
51 APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEPRGPEPDDETELRPR 100

101 GRSLV IISTLDGRIAALDPENHGKKQWDL DVGGS LVSSSLSKPEVFGNK 150
  |||||
101 GRSLV IISTLDGRIAALDPENHGKKQWDL DVGGS LVSSSLSKPEVFGNK 150

151 MIIPSLD GALFQWDRDRDRESMETVPFTVESL LESSYKFGDDVVLVGGKSLT 200
  |||||
151 MIIPSLD GALFQWDRDRDRESMETVPFTVESL LESSYKFGDDVVLVGGKSLT 200

```

FIG. 71

```

201 TYGLSAYSGKVR·YIC·SALGCRQWSD·DEMEQEED·ILL·QRTQKT·VR·AVGPR 250
|||||
201 TYGLSAYSGKVR·YIC·SALGCRQWSD·DEMEQEED·ILL·QRTQKT·VR·AVGPR 250
|||||

251 SGNEKWN·FSVGH·FELRY·IPDMET·TRAG·FIEST·FKPN·ENTEES·KII·SD·VEEQ 300
|||||
251 SGNEKWN·FSVGH·FELRY·IPDMET·TRAG·FIEST·FKPN·ENTEES·KII·SD·VEEQ 300
|||||

301 EAAIM·DIVIK·VS·ADVAD·WKVMA·FSK·KG·GHLEWEY·QFCT·PIASAW·LLKDGKVI 350
|||||
301 EAAIM·DIVIK·VS·ADVAD·WKVMA·FSK·KG·GHLEWEY·QFCT·PIASAW·LLKDGKVI 350
|||||

351 PISLFDD·TSY·TSNDD·VLEDEE·DIVEA·ARGATENS·VYLG·MYRG·QLYL·QSSV 400
|||||
351 PISLFDD·TSY·TSNDD·VLEDEE·DIVEA·ARGATENS·VYLG·MYRG·QLYL·QSSV 400
|||||

401 RISEK·FPSSPKALE·SVTNENAI·IPL·TIKW·KPLIH·SPSRT·PVL·VGSD·DEFD 450
|||||
401 RISEK·FPSSPKALE·SVTNENAI·IPL·TIKW·KPLIH·SPSRT·PVL·VGSD·DEFD 450
|||||

```

FIG. 71 (CONT.¹)

```

      . . . . .
451 KCLSNDFSHSEYSNGALSILQYPYDNGYLYLPYKRNKRSTQITVRFL 500
      |||||
451 KCLSNDFSHSEYSNGALSILQYPYDNGYLYLPYKRNKRSTQITVRFL 500

      . . . . .
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
      |||||
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550

      . . . . .
551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600
      |||||
551 RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR 600

      . . . . .
601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
      |||||
601 GGFGVVF EAKNKVDDCN YAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650

      . . . . .
651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRRM D 700
      |||||
651 VRYFNAWLEAPPEKWQEKMD EIW LKDESTDWPLSSPSPMDAPSVKIRRM D 700

```

FIG. 71 (CONT.²)

FIG. 71 (CONT.³)

FIG. 72

210 210
251 VVLTTPPMKMVTEIAPLGSLDLRLRKHQGHFLGLTSRYAVQVAEGMGYLE 300
210 210
301 SKRFIHRDLAARNLLLATRDLVKIGDFGLMRALPQNDHYYVMQEHKVPF 350
210 210
351 AWCAPESLKTRTFSHASDTWMFGVTLWEMFTYGQEPWIGLNGSILHKID 400
210 210
401 KEGERLPRPEDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLLEAQPTDMR 450
.....

FIG. 72 (CONT.¹)

```

210 ..... 210
451 ALQDFEFPDKLHIQMNDVITVIEGRAENYWWRGQNTRTLVCVGFPRNVVT 500
      .
      .
      .
210 ..... 210
210 ..... 550
501 SVAGLSAQDISQPLQNSFIHTGHGDS DPRHCWGFPDRIDELYLGNPMDPP 550
      .
      .
      .
211 ..... PPQPAFFTQKPTYDPVSEDQDPLSSDFKRLGLRKPGGLPR 249
      ||| ::|||
551 DLLSVELSTSRPPQHLGGVKKPTYDPVSEDQDPLSSDFKRLGLRKPGGLPR 600
      .
      .
      .
250 GLWLAKPSARVPGTKASRGSGAEVTLIDFGEEPVPALRPCAPSLAQLAM 299
      |||
601 GLWLAKPSARVPGTKASRGSGAEVTLIDFGEEPVP...PYGPAALPGAA 647
      .
      .
      .
300 DACSL...DETPPQSPTRALPRPLHPTPVVDWDARPLPPPAYDDVAQDE 347
      || :| ::| :|
648 GHGRLLPAGRDPASEPHAGTARPLHPTPVVDWDARPLPPPAYDDVAQDE 697

```

FIG. 72 (CONT.²)

FIG. 72 (CONT.³)

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FIG. 72 (CONT.⁴)

FIG. 73

```

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350
|||||
301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCDILENVPGRSK 350

. . . . .
351 ATSVALPGWSPSETRSFMSRTSKSKGSSRNLLKTDDLSDNDVCAVLKLD 400
|||||
351 ATSVALPGWSPSETRSFMSRTSKSKGSSRNLLKTDDLSDNDVCAVLKLD 400

. . . . .
401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
|||||
401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450

. . . . .
451 LEDFLDNQRHGMCLYLEPQGTLEFAEVTFFNPVIERRPKLQRQKKIFSKQ 500
|||||
451 LEDFLDNQRHGMCLYLEPQGTLEFAEVTFFNPVIERRPKLQRQKKIFSKQ 500

. . . . .
501 GKTFRLAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||
501 GKTFRLAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550

551 IPQLAPPA 558
|||||
551 IPQLAPPA 558

```

FIG. 73 (CONT.¹)

```

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLDIFSMTMVQKLLDDIKD 50
  |||||
1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLDIFSMTMVQKLLDDIKD 50

. . .
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100
  |||||
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100

. . .
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRRLLKALQKQLDIELK 150
  |||||
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRRLLKALQKQLDIELK 150

. . .
151 VKQGAENMIQMYSGSSKDRKLHGTAQQLLDQSKTKIEVIRMQILQAVQT 200
  |||||
151 VKQGAENMIQMYSGSSKDRKLHGTAQQLLDQSKTKIEVIRMQILQAVQT 200

. . .
201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250
  |||||
201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250

```

FIG. 74


```

251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSLVA 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSLVA 300

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRLMGCQDILENVPGRSK 350
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRLMGCQDILENVPGRSK 350

351 ATSVALPGWSPSETRSSFMSRTSKSKSGSSRNLLKTDDLSNDVCAVLKLD 400
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 ATSVALPGWSPSETRSSFMSRTSKSKSGSSRNLLKTDDLSNDVCAVLKLD 400

401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEI SVYWRDWRSLCAVKFLR 450
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEI SVYWRDWRSLCAVKFLR 450

```

FIG. 74 (CONT.¹)

[illegible]

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50

51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI IEKQAGHSRVRFREVE TLYQ 100
  |||||
51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI IEKQAGHSRVRFREVE TLYQ 100

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
    |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131
    
```

FIG. 75

FIG. 76

```

1  MSGMKLNNSCTPIITPELTTPCGSAEYMAPEVVEFTDQATFYDKRCDL 50
   :|||||||||||||||||||||||||||||||||||||||||
194 LGSGMKLNNSCTPIITPELTTPCGSAEYMAPEVVEFTDQATFYDKRCDL 243

   . . . . .
51  WSLGVVLYIMLSGYPPFVGHCGADCGWDRGEVCRVCQNKLFESIQEGKYE 100
   |||||||||||||||||||||||||||||||||||||||
244 WSLGVVLYIMLSGYPPFVGHCGADCGWDRGEVCRVCQNKLFESIQEGKYE 293

   . . . . .
101 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 150
   |||||||||||||||||||||||||||||||||||||||
294 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 343

   . . . . .
151 TPQVLQRNSSTMDLTTLFAAEAIALNRQLSQHEENELAEFPEALADGLCSM 200
   |||||||||||||||||||||||||||||||||||||||
344 TPQVLQRNSSTMDLTTLFAAEAIALNRQLSQHEENELAEFPEALADGLCSM 393

   . . . . .
201 KLSPPCKSRLARRRALAQAGGEDRSPPTAL 231
   |||||||||||||||||||||||||||||||
394 KLSPPCKSRLARRRALAQAGGEDRSPPTAL 424

```

FIG. 77

```

1 MRKGVVKDPEIADLFYKDDPEELFIGLHEIGHGSGFGAVYFATNAHTSEV 50
  |||||
1 MRKGVVKDPEIADLFYKDDPEELFIGLHEIGHGSGFGAVYFATNAHTSEV 50

      .
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100

      .
101 MEYCLGSASDLLLEVHKKPLQVEIAAITHGALHGLAYLHSHALIHR 146
  |||||
101 MEYCLGSASDLLLEVHKKPLQVEIAAITHGALHGLAYLHSHALIHR 146

```

FIG. 78

```

      . . .
52 TPEKKQNDQNRNKRKAEPYETSQGKGTPRGHKISDYFETA 91
   | | | | | | | | | | | | | | | | | | | | | |
51 TPEKKQNDQNRNKRKAEPYETSQGKGTPRGHKISDYFEFA 90

```

FIG. 79

[illegible]

FIG. 80

FIG. 18

```

      .      .      .      .      .      .      .      .      .      .
269 RAHSGAAPWQPLAAPSGASAAEQIQRGPNQPVESDESLGGLSAAALRSW 318
      |||||||
553 RAHSGAAPWQPLAAPSGASAAEQIQRGPNQPVESDESLGGLSAAALRSW 602

      .      .      .      .      .      .      .      .      .      .
319 HLTSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 368
      |||||||
603 HLTSCPLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 652

      .      .      .      .      .      .      .      .      .      .
369 SSSEPPQIIINPARQKVMQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 418
      |||||||
653 SSSEPPQIIINPARQKVMQKLALYEDGALDSLQLLSSSSLPGLGLEQDRQ 702

      .
419 GPKKVMNFRA 428
      ||::: :|:::
703 GPEESDEFQS 712

```

FIG. 81 (CONT.¹)

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```

1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV 50
  |||||
1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV 50
  |||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIIT 100
  |||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADLVHILTHLQLLRARDIIT 100
  |||||
101 AWHPPAPLPSPGTTAPRPSSIIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||
101 AWHPPAPLPSPGTTAPRPSSIIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||
151 QTHSGPELGLVPSPASLWPPPPSPAPSSSTKPGPESSVSLQGARPSPCFW 200
  |||||
151 QTHSGPELGLVPSPASLWPPPPSPAPSSSTKPGPESSVSLQGARPSPCFW 200
  |||||
  
```

FIG. 82

[illegible]

FIG. 82 (CONT.¹)

1 MFTEEDVKFYLAELALALDHLHSLGIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEEDVKFYLAELALALDHLHSLGIYRDLKPENILLDEEGHIKLTDFG 213
 |||||
 51 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 100
 |||||
 214 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 263
 |||||
 101 GTLPFQGGKDRKETMTMILKAKLGMPPQFLSPEAQSLRMLFKRNPANRLGA 150
 |||||
 264 GTLPFQGGKDRKETMTMILKAKLGMPPQFLSPEAQSLRMLFKRNPANRLGA 313
 |||||
 151 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 200
 |||||
 314 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 363
 |||||
 201 KTPKDSPIPPSANAHQLFRGFSFVAITSDDDESQAMQTVGVHSIVQQLHR 250
 |||||
 364 KTPKDSPIPPSANAHQLFRGFSFVAITSDDDESQAMQTVGVHSIVQQLHR 413
 |||||
 251 NSIQFTDGYEVKEDIGVGSYVCKRCIHKATNMEFAVKV 289
 |||||
 414 NSIQFTDGYEVKEDIGVGSYVCKRCIHKATNMEFAVKI 452

FIG. 83

FIG. 84

1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGAAAVGEGEEHQLPPPP 50
|||||
1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGAAAVGEGEEHQLPPPP 50
|||||
51 PGSFWNVESAAAPGIGCPAATSSSSATRGSSVGGSRRTTVAYVINEA 100
|||||
51 PGSFWNVESAAAPGIGCPAATSSSSATRGSSVGGSRRTTVAYVINEA 100
|||||
101 SQQLVVAESEALQSLREACETVGATLETLHFGLDFGETTVLDRFYNAD 150
|||||
101 SQQLVVAESEALQSLREACETVGATLETLHFGLDFGETTVLDRFYNAD 150
|||||
151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
|||||
151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
|||||
201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMKGLTELMQPNFELLGPIC 250
|||||
201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMKGLTELMQPNFELLGPIC 250

FIG. 85

```

      .      .      .      .      .      .      .      .      .      .
251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300

      .      .      .      .      .      .      .      .      .      .
301 QRVNIEVLTADIVINLLLSYRDIQDYDSIVKLVEKLEKLPFDLASHHH 350
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 QRVNIEVLTADIVINLLLSYRDIQDYDSIVKLVEKLEKLPFDLASHHH 350

      .      .      .      .      .      .      .      .      .      .
351 VKFHYAFALNRRNLPGDRAKALDIMI PMVQSEGQVASD MYCLVGRIYKDM 400
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 VKFHYAFALNRRNLPGDRAKALDIMI PMVQSEGQVASD MYCLVGRIYKDM 400

      .      .      .      .      .      .      .      .      .      .
401 FLDSNFTDTERD HGASWFKKAF ESEPTLQSGIN YAVLLLAAGHQFESSF 450
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 FLDSNFTDTERD HGASWFKKAF ESEPTLQSGIN YAVLLLAAGHQFESSF 450

      .      .      .      .      .      .      .      .      .      .
451 ELRKVG 456
      | | | | |
451 ELRKVG 456

```

FIG. 85 (CONT.¹)

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FIG. 86

68 IGS.....AAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLKMCVN 110
||| |||||
70 IGGAQGI VCAAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLKMCVN 119
111 HKNII SLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQME LDHERMSYL 160
|||||
120 HKNII SLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQME LDHERMSYL 169
161 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 210
|||||
170 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 219
211 MTPYVVTRYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 260
|||||
220 MTPYVVTRYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 269
261 DQWNKVIEQLGTPCPEFMKKLQPTVRN YVENRPKYAGLTFPKLFPDSLFP 310
|||||
270 DQWNKVIEQLGTPCPEFMKKLQPTVRN YVENRPKYAGLTFPKLFPDSLFP 319

FIG. 87

$$\begin{array}{ccc} 411 & V\bar{Q}\bar{Q} & 413 \\ & ||| & \\ 420 & V\bar{Q}\bar{Q} & 422 \end{array}$$

FIG. 87 (CONT.¹)

```

1 MSKSKVDNQFYSEVVGDSFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 50
  |||||
39 MSKSKVDNQFYSEVVGDSFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 88
  .
51 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNV..... 85
  |||||
89 NVAIKKLSRPFQNTAKRAYRELVLKMCVNHKNIIISLLNVFTTPQKTL EE 138

86 ...SFVIFKLLAVGVCKI 100
  ::::|: ::|::
139 FQDVYLVMEI LMDANLCQV 156

```

FIG. 88

```

1 MAMTGSTPCSSMSNHTKERVMTKVTLENFYSNLIAQHEEREMRQKKLEK 50
  |||||
1 MAMTGSTPCSSMSNHTKERVMTKVTLENFYSNLIAQHEEREMRQKKLEK 50

51 VMEEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGLEDFFESLKVIGRAF 100
  |||||
51 VMEEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGLEDFFESLKVIGRAF 100

101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAEIRDILVEADSLWVV 150
  |||||
101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAEIRDILVEADSLWVV 150

151 KMFYSFQDKLNLYLIMEFLPGGDMMTLLMKKDTLTTEETQFYIAETVLAI 200
  |||||
151 KMFYSFQDKLNLYLIMEFLPGGDMMTLLMKKDTLTTEETQFYIAETVLAI 200

201 DSIHQQLGFHARDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250
  |||||
201 DSIHQQLGFHARDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250

```

FIG. 89

251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300
|||||
251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFSTVGTPDYIAPEVFMQTGYN 300
|||||
301 KLCDWWSLGVIMYEMLIG 318
|||||
301 KLCDWWSLGVIMYEMLIG 318

FIG. 89 (CONT.¹)

```

11 VSGGMLDI IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDI IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVKRKT FVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVKRKT FVGTPCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 292
.
161 PTLTGVEDKEMMKKYGKSFRLKLLSLCLQKDP SKRPTAAELLKCKFFQKA 210
|||||
293 PTLTGVEDKEMMKKYGKSFRLKLLSLCLQKDP SKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDD EMD 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDD EMD 392

```

FIG. 90

```

      .      .      .      .      .
261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQISLVHDSQGGPNA 310
      |||||
393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEIQISLVHDSQGGPNA 442
      .      .      .      .      .
311 NEDYREASSCAVNLVLRNLSRKELNDRFEFTPGRDTADGVSQELFSAG 360
      |||||
443 NEDYREASSCAVNLVLRNLSRKELNDRFEFTPGRDTADGVSQELFSAG 492
      .      .      .      .      .
361 LVDGHDVVI VAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 410
      |||||
493 LVDGHDVVI VAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 542

      411 QLSVS 415
           |||||
      543 QLSVS 547

```

FIG. 90 (CONT.¹)


```

11 VSGGMLDIIKYIVNRGEHKNVLEEAIIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIIKYIVNRGEHKNVLEEAIIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLMITLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLMITLQNDP 292
.
161 PTLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 210
|||||
293 PTLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 392

```

FIG. 91

261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 310
 ||||| 311 NEDYREASSCAVNLVLRNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
 393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 442
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKL 391
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKL 523

FIG. 91 (CONT.¹)